

**Amendments to the Claims:**

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Currently Amended) An isolated rpoB gene or gene fragment of a bacterium of the genus Streptococcus and the 4 related genera Enterococcus, Gemella, Abiotrophia and Granulicatella, characterized in that it comprises comprising a nucleic acid sequence chosen selected from the group consisting of: among sequences
  - a. SEQ ID n° 8 to 35 Nos:8-10, 13, 15-21, and 24-35 in which:
    - the K nucleotide represents T or G,
    - the M nucleotide represents A or C,
    - the R nucleotide represents A or G,
    - the W nucleotide represents A or T,
    - the Y nucleotide represents C or T, and
    - the N nucleotide represents A, T, C, G or I, and or I;
  - b. the reverse sequences and complementary sequences of the nucleic acid sequences of (a); and these
  - c. sequences having at least 98.7 % homology to the nucleic acid sequences of (a) or (b), excepting sequences SEQ ID n° 11, 12, 14 and 22.
2. (Currently Amended) An isolated rpoB gene of claim 1 wherein the bacterium is one of the bacteria of one of the bacteria Streptococcus anginosus, Streptococcus equinus, Abiotrophia defectiva and Enterococcus faecalis, as in claim 1, characterized in that comprising a nucleic acid sequence selected from the group consisting of it corresponds to one of the sequences chosen from:

a. among sequences SEQ ID n° 1 to 3 NOs:1-3 and SEQ ID n° 5 NO:5 in which wherein:

the K nucleotide represents T or G,  
the M nucleotide represents A or C,  
the R nucleotide represents A or G,  
the W nucleotide represents A or T,  
the Y nucleotide represents C or T,  
the N nucleotide represents A, T, C, G or I, and

and the reverse sequences and

b. complementary sequences of the nucleic acid sequences of (a); and those  
c. sequences having at least 98.7% homology to the nucleic acid sequences of (a) or  
(b).

3. (Currently Amended) An isolated rpoB gene fragment of a bacterium of the genus Streptococcus and of the 4 related genera Enterococcus, Gemella, Abiotrophia and Granulicatella, characterized in that its sequence is included in or comprising a nucleic acid sequence selected from the group consisting of: consists of one of sequences

(a) SEQ ID n° 8 to 35 NOs:8-35, in which:

the K nucleotide represents T or G,  
the M nucleotide represents A or C,  
the R nucleotide represents A or G,  
the W nucleotide represents A or T,  
the Y nucleotide represents C or T,  
the N nucleotide represents A, T, C or G; and

(b) and the reverse sequences and complementary sequences of the nucleic acid sequences of (a), and those

(c) sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b).

4. (Currently Amended) An isolated oligonucleotide Oligonucleotide characterized in that it comprises comprising:

(a) a sequence specific to a species of a nucleic acid sequence specific to a bacterium of genus *Streptococcus* and said 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, preferably having at least 20 consecutive nucleotides, further preferably and comprising at least 30 20-100 consecutive nucleotides included in one of said nucleic acid sequences SEQ ID n° 8 to 35 NOs:8-35, in which:

the K nucleotide represents T or G,

the M nucleotide represents A or C,

the R nucleotide represents A or G,

the W nucleotide represents A or T,

the Y nucleotide represents C or T,

the N nucleotide represents A, T, C or G

(b) and the reverse sequences and complementary sequences of the nucleic acid sequences of (a) and those

(c) sequences having at least 98.7% homology to the nucleic acid sequences of (a) or (b).

5. (Cancelled)

6. (Currently Amended) An isolated oligonucleotide Oligonucleotide characterized in that it comprises comprising a sequence of at least 8, preferably at least 12, further

~~preferably 18 to 35 nucleotide motifs nucleotides, including at least one sequence of 8 consecutive nucleotide motifs nucleotides included in one of the following sequences SEQ ID n° 6 and 7:~~

SEQ ID n° 6 NO:6: 5'- AARYTNGGM CCTGAAGAAAAT-3', and

SEQ ID n° 7 NO:7: 5'- TGNARTTTRTCATCAACC ATGTG-3'

in which:

N represents inosine or one of the 4 nucleotides A, T, C or G,

R represents A or G,

M represents A or C, and

Y represents C or T,

~~and the reverse sequences and complementary sequences thereof.~~

7. (Currently Amended) ~~Mixture~~ A mixture of oligonucleotides, characterized in that ~~it consists of~~ consisting of an equimolar mixture of oligonucleotides as defined in claim 6, ~~all~~ wherein each oligonucleotide in the mixture of oligonucleotides ~~having~~ has a different sequence and ~~all comprising~~ comprises a said sequence included in SEQ ID n° 6 NO:6 or ~~all~~ a sequence included in SEQ ID n° 7 NO:7 or complementary sequence thereof.

8. (Currently Amended) ~~Mixture~~ A mixture of oligonucleotides, characterized in that ~~it consists of~~ comprising an equimolar mixture of 32 said oligonucleotides as defined in claim 7, ~~6, wherein each oligonucleotide in the mixture of oligonucleotides has~~ having a different sequences sequence and ~~each comprising~~ comprises at least 15, ~~preferably at least 18~~ consecutive nucleotide motifs, nucleotides included in the following sequence:

SEQ ID n° 6 NO:6 5'- AARYTNGGM CCTGAAGAAAAT-3'

in which:

R represents A or G,

Y represents C or T,

M represents A or C, and

N represents A, T, C or G

and the reverse sequences and or in a complementary sequences sequence thereof.

9. (Currently Amended) MixtureA mixture of oligonucleotides, characterized in that it consists of consisting of an equimolar mixture of 8 said oligonucleotides as defined in claim-7\_6, wherein each oligonucleotide in the mixture of oligonucleotides having has a different sequences sequence and each comprising comprises at least 15, preferably at least 18 consecutive nucleotide motifs nucleotides included in the following sequence:

SEQ ID-n°6: NO:6 5'- AARYTNGGMCCCTGAAGAAAT-3'

in which:

R represents A or G,

Y represents C or T,

M represents A or C, and

N represents inosine,

and the reverse sequences and or in a complementary sequences sequence thereof.

10. (Currently Amended) MixtureA mixture of oligonucleotides characterized in that it consists of consisting of an equimolar mixture of 16 said oligonucleotides as defined in claim-7\_6, wherein each oligonucleotide in the mixture of oligonucleotides having has a different sequences sequence and each comprising comprises at least 15, preferably at least 21 consecutive nucleotide motifs nucleotides included in the following sequence:

SEQ ID-n°7: NO:7 5'- TGNARTTTRTCATCAACCATGTG-3'

in which:

R represents A or G, and

N represents A, T, C or G

~~and the reverse sequences and or in a complementary sequences sequence thereof.~~

11. (Currently Amended) ~~Mixture~~A mixture of oligonucleotides, ~~characterized in that~~  
~~it consists of~~ consisting of an equimolar mixture of 4 said oligonucleotides as defined in  
claim 7 6, wherein each oligonucleotide in the mixture of oligonucleotides ~~having~~ has a  
different sequences sequence and each comprising comprises at least 15, preferably at least 21  
consecutive nucleotide motifs nucleotides included in the following sequence:

SEQ ID n°7: NO:7      5'- TGNARTTTRTCATCAACCATGTG-3'

in which:

R represents A or G, and

N represents inosine

~~and the reverse sequences and or in a complementary sequences sequence thereof.~~

12. (Currently Amended) ~~Mixture~~A mixture of oligonucleotides, ~~as defined in claim~~  
~~7, characterized in that said sequences consist of~~ consisting of an equimolar mixture of  
oligonucleotides as defined in claim 6, wherein each oligonucleotide in the mixture of  
oligonucleotides has a different sequence consisting of said sequences sequence included in  
SEQ ID n°6 and 7 NO:6 or sequence included in SEQ ID NO:7 ~~in which, preferably, N~~  
~~represents inosine, and the reverse sequences and or complementary sequences sequence~~  
~~thereof.~~

13-14. (Cancelled)

15. (Currently Amended) ~~Method as in claim 14 in which it is sought to detect~~A  
method for detecting the presence of a bacterium of genus *Streptococcus* or of said 4 related  
genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, characterized in that it  
comprises comprising the steps in which:

1- contacting at least one genus probe comprising a-said mixture of oligonucleotides as in ~~any of claims 7 to 12~~ claim 7, is contacted with a specimen containing or possibly containing nucleic acids of at least one ~~such~~ said bacterium ~~of genus Streptococcus and its said 4 related genera~~, and

2- determining the formation or non-formation of a hybridisation complex—is determined between said genus probe and the nucleic acids of the specimen, ~~and in this way wherein~~ the presence ~~is determined~~ of said bacterium in the specimen ~~if is indicated by formation of~~ a hybridisation complex ~~is formed~~.

16. (Currently Amended) MethodA method for detecting the presence of a bacterium of genus *Streptococcus* or of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, as in ~~claim 14~~, characterized in that it comprises comprising the steps in which:

1- contacting the amplification primers comprising said mixtures of oligonucleotides as in ~~any of claims 7 to 12~~ claim 7, ~~are~~ contacted with a specimen containing or possibly containing nucleic acids of at least one ~~such~~ said bacterium ~~of genus Streptococcus and said 4 related genera~~, and with:

as 5' primer, a said mixture of oligonucleotides comprising a sequence included in SEQ ID ~~n°6~~ NO:6, ~~preferably consisting of said complete sequence SEQ ID n°6~~, or a ~~said~~ complementary sequence thereof as in any of claims 7, 8, 9 or 12, and

as 3' primer a said mixture of oligonucleotides comprising a sequence included in SEQ ID ~~n°7~~ NO:7, ~~or preferably consisting of said complete sequence SEQ ID n°7~~, or a ~~said~~ complementary sequence thereof as in any of claims 7, 10, 11 or 12.

2- ~~the amplifying nucleic acids are amplified~~ by enzymatic polymerisation reaction to determine the presence or absence of an amplification product, wherein occurrence of an amplification product indicates and in this manner the presence is determined of said bacterium in the specimen ~~if an amplification product occurs~~.

17. (Currently Amended) ~~Method as in claim 14, characterized in that it is sought to specifically detect~~ A method for detecting a given species of a bacterium in the *Streptococcus* group and ~~said~~ 4 related genera, ~~chosen selected~~ from among the species:

*Streptococcus mutans, Streptococcus oralis, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus salivarius, Streptococcus sanguinis, Streptococcus suis, Streptococcus acidominimus, Streptococcus agalactiae, Streptococcus anginosus, Streptococcus constellatus, Streptococcus difficilis, Streptococcus dysgalactiae, Streptococcus equi, Streptococcus equinus, Streptococcus intermedius, Streptococcus mitis, Streptococcus bovis, Streptococcus alactolyticus, Streptococcus galloyticus, Streptococcus macedonicus, Streptococcus infantarius, Streptococcus hominis, Granulicatella adjacens, Abiotrophia defectiva, Enterococcus avium, Enterococcus casselliflavus, Enterococcus faecalis, Enterococcus faecium, Enterococcus gallinarum, Enterococcus sacharolyticus, Gemella haemolysans, and Gemella morbillorum,*

said method in which comprising:

1- contacting a specimen containing or possibly containing nucleic acids of at least one such bacterium ~~is contacted with at least one species probe consisting of a gene or a gene fragment - as in claim 3 any of claims 1 to 3, or an oligonucleotide as in claim 4, and~~

2- determining ~~the~~ formation or non-formation ~~is determined~~ of a hybridisation complex between said probe and ~~the~~ nucleic acids of the specimen, wherein the formation of

a hybridisation complex indicates and in this way the presence of said bacterium in the sample is determined if a hybridisation complex is formed.

18. (Currently Amended) ~~Method as in claim 14, characterized in that it is sought to detect~~A method for detecting a given species of a bacterium of genus *Streptococcus* ~~and said or related genera chosen selected~~ from among the species:

*Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus suis*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus difficilis*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus equinus*, *Streptococcus intermedius*, *Streptococcus mitis*, *Streptococcus bovis*, *Streptococcus alactolyticus*, *Streptococcus galloyticus*, *Streptococcus macedonicus*, *Streptococcus infantarius*, *Streptococcus hominis*, *Granulicatella adjacens*, *Abiotrophia defectiva*, *Enterococcus avium*, *Enterococcus casselliflavus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus sacharolyticus*, *Gemella haemolysans*, and *Gemella morbillorum*, a method in which, in a specimen containing or possibly containing nucleic acids of at least one said bacterium ~~of genus~~ *Staphylococcus*, the steps are performed in which comprising:

- a) ~~a sequencing reaction is conducted of~~ an amplified *rpoB* gene fragment of a ~~said given~~ bacterium using nucleotide primers consisting of said oligonucleotide mixtures as in ~~claim 7~~any of claims 7 to 12 comprising sequences included in SEQ ID ~~n°6~~ NO:6 as 5' primer and in SEQ ID ~~n°7~~ NO:7 as 3' primer, ~~preferably sequences consisting of said sequences~~ SEQ ID ~~n°6 and 7~~, and ~~said~~ or complementary sequences thereof, and
- b) wherein the presence or absence of the given species of said bacterium is determined by comparing the sequence obtained of said fragment with the sequence of the

complete *rpoB* gene of said bacterium or the sequence of a *rpoB* gene fragment of said bacterium respectively comprising said sequences SEQ ID ~~n°8 to 35~~ NOs:8-35 as in any of claims 1 to 4 and complementary sequences thereof, wherein and in this manner the presence of said bacterium in the specimen is determined if the obtained sequence of said fragment is identical to the known sequence of the *rpoB* gene or gene fragment of said bacterium.

19. (Cancelled)

20. (New) A method as in claim 16, wherein it is sought to specifically detect a given species of a bacterium selected from the species:

*Streptococcus mutans*, *Streptococcus oralis*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Streptococcus salivarius*, *Streptococcus sanguinis*, *Streptococcus suis*, *Streptococcus acidominimus*, *Streptococcus agalactiae*, *Streptococcus anginosus*, *Streptococcus constellatus*, *Streptococcus difficile*, *Streptococcus dysgalactiae*, *Streptococcus equi*, *Streptococcus equinus*, *Streptococcus intermedius*, *Streptococcus mitis*, *Streptococcus bovis*, *Streptococcus alactolyticus*, *Streptococcus galloyticus*, *Streptococcus macedonicus*, *Streptococcus infantarius*, *Streptococcus hominis*, *Granulicatella adjacens*, *Abiotrophia defectiva*, *Enterococcus avium*, *Enterococcus casselliflavus*, *Enterococcus faecalis*, *Enterococcus faecium*, *Enterococcus gallinarum*, *Enterococcus sacharolyticus*, *Gemella haemolysans*, and *Gemella morbillorum*, further comprising steps of:

1- contacting a specimen containing or possibly containing amplified *rpoB* gene nucleic acids of at least one such bacterium, with at least one species probe consisting of a gene fragment of a bacterium of the genus *Streptococcus* and of 4 related genera *Enterococcus*, *Gemella*, *Abiotrophia* and *Granulicatella*, comprising a nucleic acid sequence selected from the group consisting of:

(a) SEQ ID NOs:8-35, in which:

K nucleotide represents T or G,

M nucleotide represents A or C,

R nucleotide represents A or G,

W nucleotide represents A or T,

Y nucleotide represents C or T,

N nucleotide represents A, T, C or G; and

(b) complementary sequences of the nucleic acid sequences of (a), and

(c) sequences having at least 98.7% homology to the nucleic acid sequences of (a) or

(b), and

2- determining formation or non-formation of a hybridisation complex between said probe and the nucleic acids of the specimen, wherein the formation of a hybridisation complex indicates the presence of said bacterium in the sample.

21. (New) An isolated oligonucleotide of claim 6, wherein said sequence has 18-35 nucleotides.